



SEQUENCE LISTING

<110> Gish, Kurt C.  
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Eos Biotechnology, Inc.

<120> Uses of PBH1 in the Diagnosis and Therapeutic Treatment  
of Prostate Cancer

<130> 018501-005910US

<140> US 10/058,513  
<141> 2002-01-24

<150> US 60/263,951  
<151> 2001-01-24

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<170> PatentIn Ver. 2.1

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Gly Thr Pro Gln Gly Leu Pro Val Pro Ile Ser Glu Gly Ser Met Lys  
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Ser Phe Leu Pro Val His Thr Ile Val Leu Ile Arg Glu Asn Val Cys  
                   50                  55                  60

Lys Cys Gly Tyr Ala Gln Ser Gln His Met Glu Gly Thr Gln Ile Asn  
                   65                  70                  75                  80

Gln Ser Glu Lys Trp Asn Tyr Lys Lys His Thr Lys Glu Phe Pro Thr  
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Asp Ala Phe Gly Asp Ile Gln Phe Glu Thr Leu Gly Lys Lys Gly Lys  
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Tyr Ile Arg Leu Ser Cys Asp Thr Asp Ala Glu Ile Leu Tyr Glu Leu  
                   115                  120                  125

Leu Thr Gln His Trp His Leu Lys Thr Pro Asn Leu Val Ile Ser Val  
                   130                  135                  140

Thr Gly Gly Ala Lys Asn Phe Ala Leu Lys Pro Arg Met Arg Lys Ile  
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Phe Ser Arg Leu Ile Tyr Ile Ala Gln Ser Lys Gly Ala Trp Ile Leu  
                   165                  170                  175

Thr Gly Gly Thr His Tyr Gly Leu Met Lys Tyr Ile Gly Glu Val Val  
                   180                  185                  190

Arg Asp Asn Thr Ile Ser Arg Ser Ser Glu Glu Asn Ile Val Ala Ile  
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Gly Ile Ala Ala Trp Gly Met Val Ser Asn Arg Asp Thr Leu Ile Arg  
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Asn Cys Asp Ala Glu Gly Tyr Phe Leu Ala Gln Tyr Leu Met Asp Asp  
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Phe Thr Arg Asp Pro Leu Tyr Ile Leu Asp Asn Asn His Thr His Leu  
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                   275                  280                  285

Ser Asn Tyr Gly Gly Lys Ile Pro Ile Val Cys Phe Ala Gln Gly Gly  
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Gly Lys Glu Thr Leu Lys Ala Ile Asn Thr Ser Ile Lys Asn Lys Ile  
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Pro Cys Val Val Val Glu Gly Ser Gly Gln Ile Ala Asp Val Ile Ala  
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Lys Leu Val Arg Phe Leu Pro Arg Thr Val Ser Arg Leu Pro Glu Glu  
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Glu Thr Glu Ser Trp Ile Lys Trp Leu Lys Glu Ile Leu Glu Cys Ser  
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His Leu Leu Thr Val Ile Lys Met Glu Glu Ala Gly Asp Glu Ile Val  
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Ser Asn Ala Ile Ser Tyr Ala Leu Tyr Lys Ala Phe Ser Thr Ser Glu  
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Gln Asp Lys Asp Asn Trp Asn Gly Gln Leu Lys Leu Leu Leu Glu Trp  
420 425 430

Asn Gln Leu Asp Leu Ala Asn Asp Glu Ile Phe Thr Asn Asp Arg Arg  
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Trp Glu Lys Ser Lys Pro Arg Leu Arg Asp Thr Ile Ile Gln Val Thr  
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Trp Leu Glu Asn Gly Arg Ile Lys Val Glu Ser Lys Asp Val Thr Asp  
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Gly Lys Ala Ser Ser His Met Leu Val Val Leu Lys Ser Ala Asp Leu  
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Gln Glu Val Met Phe Thr Ala Leu Ile Lys Asp Arg Pro Lys Phe Val  
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Arg Leu Phe Leu Glu Asn Gly Leu Asn Leu Arg Lys Phe Leu Thr His  
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Asp Val Leu Thr Glu Leu Phe Ser Asn His Phe Ser Thr Leu Val Tyr  
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Arg Asn Leu Gln Ile Ala Lys Asn Ser Tyr Asn Asp Ala Leu Leu Thr  
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Phe Val Trp Lys Leu Val Ala Asn Phe Arg Arg Gly Phe Arg Lys Glu  
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Asp Arg Asn Gly Arg Asp Glu Met Asp Ile Glu Leu His Asp Val Ser  
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Pro Ile Thr Arg His Pro Leu Gln Ala Leu Phe Ile Trp Ala Ile Leu  
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Gln Asn Lys Lys Glu Leu Ser Lys Val Ile Trp Glu Gln Thr Arg Gly  
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 Ala Arg Pro Gly Ser Arg Ser Arg His Ser Phe His Thr Ser Leu Gln  
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 Ala Glu Gly Ala Ser Ser Gly Leu Gly Gln Pro Arg Lys Gly Leu Pro  
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 Thr Leu Gly Leu Phe Tyr Phe Ile Ala Gly Ile Val Phe Arg Leu His  
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Ser Ser Asn Lys Ser Ser Leu Tyr Ser Gly Arg Val Ile Phe Cys Leu  
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 Asp Tyr Ile Ile Phe Thr Leu Arg Leu Ile His Ile Phe Thr Val Ser  
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 Leu Ala Met Phe Gly Gln Val Pro Ser Asp Val Asp Gly Thr Thr Tyr  
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 Gly Ser Lys Glu Leu Phe Gly Ser Gln Cys Ala Leu Met Leu Val Phe  
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 Gly Lys Tyr Ile Arg Leu Ser Cys Asp Thr Asp Ala Glu Ile Leu Tyr  
 50 55 60  
 Glu Leu Leu Thr Gln His Trp His Leu Lys Thr Pro Asn Leu Val Ile  
 65 70 75 80  
 Ser Val Thr Gly Ala Lys Asn Phe Ala Leu Lys Pro Arg Met Arg  
 85 90 95  
 Lys Ile Phe Ser Arg Leu Ile Tyr Ile Ala Gln Ser Lys Gly Ala Trp  
 100 105 110  
 Ile Leu Thr Gly Gly Thr His Tyr Gly Leu Met Lys Tyr Ile Gly Glu  
 115 120 125  
 Val Val Arg Asp Asn Thr Ile Ser Arg Ser Ser Glu Glu Asn Ile Val  
 130 135 140  
 Ala Ile Gly Ile Ala Ala Trp Gly Met Val Ser Asn Arg Asp Thr Leu  
 145 150 155 160

Ile Arg Asn Cys Asp Ala Glu Gly Tyr Phe Leu Ala Gln Tyr Leu Met  
 165 170 175  
 Asp Asp Phe Thr Arg Asp Pro Leu Tyr Ile Leu Asp Asn Asn His Thr  
 180 185 190  
 His Leu Leu Leu Val Asp Asn Gly Cys His Gly His Pro Thr Val Glu  
 195 200 205  
 Ala Lys Leu Arg Asn Gln Leu Glu Lys Tyr Ile Ser Glu Arg Thr Ile  
 210 215 220  
 Gln Asp Ser Asn Tyr Gly Gly Lys Ile Pro Ile Val Cys Phe Ala Gln  
 225 230 235 240  
 Gly Gly Gly Lys Glu Thr Leu Lys Ala Ile Asn Thr Ser Ile Lys Asn  
 245 250 255  
 Lys Ile Pro Cys Val Val Glu Gly Ser Gly Gln Ile Ala Asp Val  
 260 265 270  
 Ile Ala Ser Leu Val Glu Val Glu Asp Ala Leu Thr Ser Ser Ala Val  
 275 280 285  
 Lys Glu Lys Leu Val Arg Phe Leu Pro Arg Thr Val Ser Arg Leu Pro  
 290 295 300  
 Glu Glu Glu Thr Glu Ser Trp Ile Lys Trp Leu Lys Glu Ile Leu Glu  
 305 310 315 320  
 Cys Ser His Leu Leu Thr Val Ile Lys Met Glu Glu Ala Gly Asp Glu  
 325 330 335  
 Ile Val Ser Asn Ala Ile Ser Tyr Ala Leu Tyr Lys Ala Phe Ser Thr  
 340 345 350  
 Ser Glu Gln Asp Lys Asp Asn Trp Asn Gly Gln Leu Lys Leu Leu Leu  
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 Arg Arg Trp Glu Lys Ser Lys Pro Arg Leu Arg Asp Thr Ile Ile Gln  
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 Thr Asp Gly Lys Ala Ser Ser His Met Leu Val Val Leu Lys Ser Ala  
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 465 470 475 480

Val Tyr Arg Asn Leu Gln Ile Ala Lys Asn Ser Tyr Asn Asp Ala Leu  
 485 490 495  
 Leu Thr Phe Val Trp Lys Leu Val Ala Asn Phe Arg Arg Gly Phe Arg  
 500 505 510  
 Lys Glu Asp Arg Asn Gly Arg Asp Glu Met Asp Ile Glu Leu His Asp  
 515 520 525  
 Val Ser Pro Ile Thr Arg His Pro Leu Gln Ala Leu Phe Ile Trp Ala  
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 Arg Gly Cys Thr Leu Ala Ala Leu Gly Ala Ser Lys Leu Leu Lys Thr  
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 580 585 590  
 Leu Ala Asn Glu Tyr Glu Thr Arg Ala Val Glu Leu Phe Thr Glu Cys  
 595 600 605  
 Tyr Ser Ser Asp Glu Asp Leu Ala Glu Gln Leu Leu Val Tyr Ser Cys  
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 receptor potential-related channel 7 (TRPC7)  
 peptide sequence

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 35 40 45  
 Ser Gln Lys Val Lys Lys Tyr Val Arg Val Ser Gln Asp Thr Pro Ser  
 50 55 60  
 Ser Val Ile Tyr His Leu Met Thr Gln His Trp Gly Leu Asp Val Pro  
 65 70 75 80

Asn Leu Leu Ile Ser Val Thr Gly Gly Ala Lys Asn Phe Asn Met Lys  
 85 90 95  
 Pro Arg Leu Lys Ser Ile Phe Arg Arg Gly Leu Val Lys Val Ala Gln  
 100 105 110  
 Thr Thr Gly Ala Trp Ile Ile Thr Gly Gly Ser His Thr Gly Val Met  
 115 120 125  
 Lys Gln Val Gly Glu Ala Val Arg Asp Phe Ser Leu Ser Ser Ser Tyr  
 130 135 140  
 Lys Glu Gly Glu Leu Ile Thr Ile Gly Val Ala Thr Trp Gly Thr Val  
 145 150 155 160  
 His Arg Arg Glu Gly Leu Ile His Pro Thr Gly Ser Phe Pro Ala Glu  
 165 170 175  
 Tyr Ile Leu Asp Glu Asp Gly Gln Gly Asn Leu Thr Cys Leu Asp Ser  
 180 185 190  
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 195 200 205  
 Gly Val Glu Ile Pro Leu Arg Thr Arg Leu Glu Lys Phe Ile Ser Glu  
 210 215 220  
 Gln Thr Lys Glu Arg Gly Gly Val Ala Ile Lys Ile Pro Ile Val Cys  
 225 230 235 240  
 Val Val Leu Glu Gly Gly Pro Gly Thr Leu His Thr Ile Asp Asn Ala  
 245 250 255  
 Thr Thr Asn Gly Thr Pro Cys Val Val Val Glu Gly Ser Gly Arg Val  
 260 265 270  
 Ala Asp Val Ile Ala Gln Val Ala Asn Leu Pro Val Ser Asp Ile Thr  
 275 280 285  
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 290 295 300  
 Glu Thr Phe Thr Glu Ser Arg Ile Val Glu Trp Thr Lys Lys Ile Gln  
 305 310 315 320  
 Asp Ile Val Arg Arg Gln Leu Leu Thr Val Phe Arg Glu Gly Lys  
 325 330 335  
 Asp Gly Gln Gln Asp Val Asp Val Ala Ile Leu Gln Ala Leu Lys  
 340 345 350  
 Ala Ser Arg Ser Gln Asp His Phe Gly His Glu Asn Trp Asp His Gln  
 355 360 365  
 Leu Lys Leu Ala Val Ala Trp Asn Arg Val Asp Ile Ala Arg Ser Glu  
 370 375 380  
 Ile Phe Met Asp Glu Trp Gln Trp Lys Pro Ser Asp Leu His Pro Thr  
 385 390 395 400

Met Thr Ala Ala Leu Ile Ser Asn Lys Pro Glu Phe Val Lys Leu Phe  
 405 410 415  
 Leu Glu Asn Gly Val Gln Leu Lys Glu Phe Val Thr Trp Asp Thr Leu  
 420 425 430  
 Leu Tyr Leu Tyr Glu Asn Leu Asp Pro Ser Cys Leu Phe His Ser Lys  
 435 440 445  
 Leu Gln Lys Val Leu Val Glu Asp Pro Glu Arg Pro Ala Cys Ala Pro  
 450 455 460  
 Ala Ala Pro Arg Leu Gln Met His His Val Ala Gln Val Leu Arg Glu  
 465 470 475 480  
 Leu Leu Gly Asp Phe Thr Gln Pro Leu Tyr Pro Arg Pro Arg His Asn  
 485 490 495  
 Asp Arg Leu Arg Leu Leu Leu Pro Val Pro His Val Lys Leu Asn Val  
 500 505 510  
 Gln Gly Val Ser Leu Arg Ser Leu Tyr Lys Arg Ser Ser Gly His Val  
 515 520 525  
 Thr Phe Thr Met Asp Pro Ile Arg Asp Leu Leu Ile Trp Ala Ile Val  
 530 535 540  
 Gln Asn Arg Arg Glu Leu Ala Gly Ile Ile Trp Ala Gln Ser Gln Asp  
 545 550 555 560  
 Cys Ile Ala Ala Ala Leu Ala Cys Ser Lys Ile Leu Lys Glu Leu Ser  
 565 570 575  
 Lys Glu Glu Glu Asp Thr Asp Ser Ser Glu Glu Met Leu Ala Leu Ala  
 580 585 590  
 Glu Glu Tyr Glu His Arg Ala Ile Gly Val Phe Thr Glu Cys Tyr Arg  
 595 600 605  
 Lys Asp Glu Glu Arg Ala Gln Lys Leu Leu Thr Arg Val Ser Glu Ala  
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 Trp Gly Lys Thr Thr Cys Leu Gln Leu Ala Leu Glu Ala Lys Asp Met  
 625 630 635 640  
 Lys Phe Val Ser His Gly Gly Ile Gln  
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<210> 5  
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 <212> PRT  
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 <223> Description of Artificial Sequence:consensus  
 peptide sequence from PBH1 and TRPC7 alignment

<400> 5  
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 1 5

<210> 6  
<211> 4  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:consensus  
peptide sequence from PBH1 and TRPC7 alignment

<400> 6  
Thr Gln His Trp  
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<210> 7  
<211> 10  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:consensus  
peptide sequence from PBH1 and TRPC7 alignment

<400> 7  
Ile Ser Val Thr Gly Gly Ala Lys Asn Phe  
1 5 10

<210> 8  
<211> 4  
<212> PRT  
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<220>  
<223> Description of Artificial Sequence:consensus  
peptide sequence from PBH1 and TRPC7 alignment

<400> 8  
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<210> 9  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:consensus  
peptide sequence from PBH1 and TRPC7 alignment

<400> 9  
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1 5

<210> 10  
<211> 9  
<212> PRT  
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<220>  
<223> Description of Artificial Sequence:consensus  
peptide sequence from PBH1 and TRPC7 alignment

<400> 10  
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1 5

<210> 11  
<211> 5  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:consensus  
peptide sequence from PBH1 and TRPC7 alignment

<400> 11  
Ala Asp Val Ile Ala  
1 5

<210> 12  
<211> 4  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:consensus  
peptide sequence from PBH1 and TRPC7 alignment

<400> 12  
Leu Leu Thr Val  
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<210> 13  
<211> 4  
<212> PRT  
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<220>  
<223> Description of Artificial Sequence:consensus  
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<400> 13  
Gln Leu Lys Leu  
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<210> 14  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:consensus  
peptide sequence from PBH1 and TRPC7 alignment

<400> 14  
Leu Phe Leu Glu Asn Gly  
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<210> 15  
<211> 4  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:consensus  
peptide sequence from PBH1 and TRPC7 alignment

<400> 15  
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<210> 16  
<211> 5  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:consensus  
peptide sequence from PBH1 and TRPC7 alignment

<400> 16  
Phe Thr Glu Cys Tyr  
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<210> 17  
<211> 4  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:consensus  
peptide sequence from PBH1 and TRPC7 alignment

<400> 17  
Glu Ala Trp Gly  
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<210> 18  
<211> 57  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:PBH1 peptide  
sequence

<400> 18  
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1 5 10 15

Tyr Ile Ala Phe Leu Leu Leu Phe Ala Tyr Val Leu Leu Met Asp Phe  
20 25 30

His Ser Val Pro His Pro Pro Glu Leu Val Leu Tyr Ser Leu Val Phe  
35 40 45

Val Leu Phe Cys Asp Glu Val Arg Gln  
50 55

<210> 19  
<211> 57  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:transient  
receptor potential-related channel 7 (TRPC7)  
peptide sequence

<400> 19  
Ala Phe Phe Thr Ala Pro Val Val Val Phe His Leu Asn Ile Leu Ser  
1 5 10 15

Tyr Phe Ala Phe Leu Cys Leu Phe Ala Tyr Val Leu Met Val Asp Phe  
20 25 30

Gln Pro Val Pro Ser Trp Cys Glu Cys Ala Ile Tyr Leu Trp Leu Phe  
35 40 45

Ser Leu Val Cys Glu Glu Met Arg Gln  
50 55

<210> 20  
<211> 4  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:consensus  
peptide sequence from PBH1 and TRPC7 alignment

<400> 20  
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<210> 21  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:consensus  
peptide sequence from PBH1 and TRPC7 alignment

<400> 21  
Leu Phe Ala Tyr Val Leu  
1 5

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<210> 22
<211> 225
<212> PRT
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<220>
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<220>
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<223> Xaa = low complexity amino acid from BLASTP search

<400> 22
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Phe Ile Ala Gly Ile Val Phe Arg Leu His Ser Ser Asn Lys Ser Ser
  20          25          30

Leu Tyr Ser Gly Arg Val Ile Phe Cys Leu Asp Tyr Ile Ile Phe Thr
  35          40          45

Leu Arg Leu Ile His Ile Phe Thr Val Ser Arg Asn Leu Gly Pro Lys
  50          55          60

Ile Ile Met Leu Gln Arg Met Thr Ser Ile Glu Met Xaa Xaa Xaa Xaa
  65          70          75          80

Xaa Xaa Ile Pro Thr Leu Arg Phe Phe Glu Phe Val Val Leu Ile Gln
  85          90          95

Ser Ile Ser Gly Thr Ser Ser His His Glu Val Met Leu Ser Asp Arg
  100         105         110

Cys Val Leu Leu Pro Val Pro Leu Cys Gly Val Asp Gly Gly Leu Cys
  115         120         125

Val Ala Arg Gln Gly Ile Leu Arg Gln Asn Glu Gln Arg Trp Arg Trp
  130         135         140

Ile Phe Arg Ser Val Ile Tyr Glu Pro Tyr Leu Ala Met Phe Gly Gln
  145         150         155         160

Val Pro Ser Asp Val Asp Gly Thr Thr Tyr Asp Phe Ala His Cys Thr
  165         170         175

Phe Thr Gly Asn Glu Ser Lys Pro Leu Cys Val Glu Leu Asp Glu His
  180         185         190

Asn Leu Pro Arg Phe Pro Glu Trp Ile Thr Ile Pro Leu Val Cys Ile
  195         200         205

Tyr Met Leu Ser Thr Asn Ile Leu Leu Val Asn Leu Leu Val Ala Met
  210         215         220

Phe
225

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<210> 23  
<211> 186  
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<220>  
<223> Description of Artificial Sequence:transient receptor potential-related channel 7 (TRPC7) peptide sequence

<400> 23  
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Phe Val Ala Gly Leu Thr Cys Arg Leu Ile Pro Ala Thr Leu Tyr Pro  
20 25 30  
  
Gly Arg Val Ile Leu Ser Leu Asp Phe Ile Leu Phe Cys Leu Arg Leu  
35 40 45  
  
Met His Ile Phe Thr Ile Ser Lys Thr Leu Gly Pro Lys Ile Ile  
50 55 60  
  
Val Lys Arg Met Met Lys Asp Val Phe Phe Leu Phe Leu Leu Ala  
65 70 75 80  
  
Val Trp Val Val Ser Phe Gly Val Ala Lys Gln Ala Ile Leu Ile His  
85 90 95  
  
Asn Glu Arg Arg Val Asp Trp Leu Phe Arg Gly Ala Val Tyr His Ser  
100 105 110  
  
Tyr Leu Thr Ile Phe Gly Gln Ile Pro Gly Tyr Ile Asp Gly Val Asn  
115 120 125  
  
Phe Asn Pro Glu His Cys Ser Pro Asn Gly Thr Asp Pro Tyr Lys Pro  
130 135 140  
  
Lys Cys Pro Glu Ser Asp Ala Thr Gln Gln Arg Pro Ala Phe Pro Glu  
145 150 155 160  
  
Trp Leu Thr Val Leu Leu Leu Cys Leu Tyr Leu Leu Phe Thr Asn Ile  
165 170 175  
  
Leu Leu Leu Asn Leu Leu Ile Ala Met Phe  
180 185

<210> 24  
<211> 4  
<212> PRT  
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<220>  
<223> Description of Artificial Sequence:consensus peptide sequence from PBH1 and TRPC7 alignment

<400> 24  
Gly Arg Val Ile  
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<210> 25  
<211> 4  
<212> PRT  
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<220>  
<223> Description of Artificial Sequence:consensus  
peptide sequence from PBH1 and TRPC7 alignment

<400> 25  
His Ile Phe Thr  
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<210> 26  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:consensus  
peptide sequence from PBH1 and TRPC7 alignment

<400> 26  
Leu Gly Pro Lys Ile Ile  
1 5

<210> 27  
<211> 4  
<212> PRT  
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<220>  
<223> Description of Artificial Sequence:consensus  
peptide sequence from PBH1 and TRPC7 alignment

<400> 27  
Phe Pro Glu Trp  
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<210> 28  
<211> 5  
<212> PRT  
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<220>  
<223> Description of Artificial Sequence:consensus  
peptide sequence from PBH1 and TRPC7 alignment

<400> 28  
Thr Asn Ile Leu Leu  
1 5

<210> 29  
<211> 45  
<212> PRT  
<213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:PBH1 peptide  
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<400> 29  
 Tyr Thr Val Gly Thr Val Gln Glu Asn Asn Asp Gln Val Trp Lys Phe  
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Gln Arg Tyr Phe Leu Val Gln Glu Tyr Cys Ser Arg Leu Asn Ile Pro  
 20 25 30

Phe Pro Phe Ile Val Phe Ala Tyr Phe Tyr Met Val Val  
 35 40 45

<210> 30  
 <211> 45  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:transient  
 receptor potential-related channel 7 (TRPC7)  
 peptide sequence

<400> 30  
 Tyr Thr Phe Gln Gln Val Gln Glu His Thr Asp Gln Ile Trp Lys Phe  
 1 5 10 15

Gln Arg His Asp Leu Ile Glu Glu Tyr His Gly Arg Pro Ala Ala Pro  
 20 25 30

Pro Pro Phe Ile Leu Leu Ser His Leu Gln Leu Phe Ile  
 35 40 45

<210> 31  
 <211> 5  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:consensus  
 peptide sequence for PBH1 and TRPC7 alignment

<400> 31  
 Trp Lys Phe Gln Arg  
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<210> 32  
 <211> 2181  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <223> exons 1-15 of PBH1

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caacacaagg ggagcacagg aacacctcg ggtcttccag ttcccatctc agaaggctca 180  
 atgaaatcc tccttcctgt ccacaccatc gtgttatca gggagaatgt gtgcagtgt 240  
 ggctatgcc agagccagca catggaaggc acccagatca accaaagtga gaaatggAAC 300  
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 gatgctgagg gctattttt agcccgatc cttatggatg acttcacaa agatccactg 780  
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 ttcactgagt gttacagcag cgatgaagac ttggcagaac agctgtgtt ctattcctgt 2100  
 gaagcttggg gtggaaagcaa ctgtctggag ctggcgggtgg aggccacaga ccagcatttc 2160  
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 <212> DNA  
 <213> Homo sapiens

<220>  
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 cacctcccccc ttctgtgtct ttccttgcgaa tttgtgtcttacatcgctt tcctcctgt 180  
 gtttgccttac gtgctgcttca tggatttcca ttccggtgcac caccctcccg agctggtcct 240  
 gtactcgctg gtctttgtcc ttttctgtga tgaagtgaga cag 283

<210> 34  
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<220>  
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<400> 34

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 acggcccggcc ccgggttcccg ctcacgcac tccttccaca cttccctgca agctgagggt 180  
 gccagctctg gccttggcca gcccagaaag gggctccac agtgcagcgg tgggctgaag 240  
 ggctcctcaa gtgcccggaa agtggggagcc caggcagagg aggtgcccag agcaagcgg 300  
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 agcagaaaact taggacccaa gattataatg ctgcagaggg tgacgagcat tgagatgagc 660  
 tcatctggaa gctccattcc aacactgagg ttctttgagt ttgtgggtt aattcaaagc 720  
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<211> 713

<212> PRT

<213> Homo sapiens

<220>

<223> exons 1-15 of PBH1

<400> 35

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														30	
				20				25							

Gly	Thr	Pro	Gln	Gly	Leu	Pro	Val	Pro	Ile	Ser	Glu	Gly	Ser	Met	Lys
														45	
					35			40							

Ser	Phe	Leu	Pro	Val	His	Thr	Ile	Val	Leu	Ile	Arg	Glu	Asn	Val	Cys
															50
								55				60			

Lys	Cys	Gly	Tyr	Ala	Gln	Ser	Gln	His	Met	Glu	Gly	Thr	Gln	Ile	Asn
														65	
									70			75			80

Gln	Ser	Glu	Lys	Trp	Asn	Tyr	Lys	Lys	His	Thr	Lys	Glu	Phe	Pro	Thr
															85
									90						95

Asp Ala Phe Gly Asp Ile Gln Phe Glu Thr Leu Gly Lys Lys Gly Lys  
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Tyr Ile Arg Leu Ser Cys Asp Thr Asp Ala Glu Ile Leu Tyr Glu Leu  
 115 120 125

Leu Thr Gln His Trp His Leu Lys Thr Pro Asn Leu Val Ile Ser Val  
 130 135 140

Thr Gly Gly Ala Lys Asn Phe Ala Leu Lys Pro Arg Met Arg Lys Ile  
 145 150 155 160

Phe Ser Arg Leu Ile Tyr Ile Ala Gln Ser Lys Gly Ala Trp Ile Leu  
 165 170 175

Thr Gly Gly Thr His Tyr Gly Leu Met Lys Tyr Ile Gly Glu Val Val  
 180 185 190

Arg Asp Asn Thr Ile Ser Arg Ser Ser Glu Glu Asn Ile Val Ala Ile  
 195 200 205

Gly Ile Ala Ala Trp Gly Met Val Ser Asn Arg Asp Thr Leu Ile Arg  
 210 215 220

Asn Cys Asp Ala Glu Gly Tyr Phe Leu Ala Gln Tyr Leu Met Asp Asp  
 225 230 235 240

Phe Thr Arg Asp Pro Leu Tyr Ile Leu Asp Asn Asn His Thr His Leu  
 245 250 255

Leu Leu Val Asp Asn Gly Cys His Gly His Pro Thr Val Glu Ala Lys  
 260 265 270

Leu Arg Asn Gln Leu Glu Lys Tyr Ile Ser Glu Arg Thr Ile Gln Asp  
 275 280 285

Ser Asn Tyr Gly Gly Lys Ile Pro Ile Val Cys Phe Ala Gln Gly Gly  
 290 295 300

Gly Lys Glu Thr Leu Lys Ala Ile Asn Thr Ser Ile Lys Asn Lys Ile  
 305 310 315 320

Pro Cys Val Val Val Glu Gly Ser Gly Gln Ile Ala Asp Val Ile Ala  
 325 330 335

Ser Leu Val Glu Val Glu Asp Ala Leu Thr Ser Ser Ala Val Lys Glu  
 340 345 350

Lys Leu Val Arg Phe Leu Pro Arg Thr Val Ser Arg Leu Pro Glu Glu  
 355 360 365

Glu Thr Glu Ser Trp Ile Lys Trp Leu Lys Glu Ile Leu Glu Cys Ser  
 370 375 380

His Leu Leu Thr Val Ile Lys Met Glu Glu Ala Gly Asp Glu Ile Val  
 385 390 395 400

Ser Asn Ala Ile Ser Tyr Ala Leu Tyr Lys Ala Phe Ser Thr Ser Glu  
 405 410 415

Gln Asp Lys Asp Asn Trp Asn Gly Gln Leu Lys Leu Leu Leu Glu Trp  
 420 425 430

Asn Gln Leu Asp Leu Ala Asn Asp Glu Ile Phe Thr Asn Asp Arg Arg  
 435 440 445

Trp Glu Lys Ser Lys Pro Arg Leu Arg Asp Thr Ile Ile Gln Val Thr  
 450 455 460

Trp Leu Glu Asn Gly Arg Ile Lys Val Glu Ser Lys Asp Val Thr Asp  
 465 470 475 480

Gly Lys Ala Ser Ser His Met Leu Val Val Leu Lys Ser Ala Asp Leu  
 485 490 495

Gln Glu Val Met Phe Thr Ala Leu Ile Lys Asp Arg Pro Lys Phe Val  
 500 505 510

Arg Leu Phe Leu Glu Asn Gly Leu Asn Leu Arg Lys Phe Leu Thr His  
 515 520 525

Asp Val Leu Thr Glu Leu Phe Ser Asn His Phe Ser Thr Leu Val Tyr  
 530 535 540

Arg Asn Leu Gln Ile Ala Lys Asn Ser Tyr Asn Asp Ala Leu Leu Thr  
 545 550 555 560

Phe Val Trp Lys Leu Val Ala Asn Phe Arg Arg Gly Phe Arg Lys Glu  
 565 570 575

Asp Arg Asn Gly Arg Asp Glu Met Asp Ile Glu Leu His Asp Val Ser  
 580 585 590

Pro Ile Thr Arg His Pro Leu Gln Ala Leu Phe Ile Trp Ala Ile Leu  
 595 600 605

Gln Asn Lys Lys Glu Leu Ser Lys Val Ile Trp Glu Gln Thr Arg Gly  
 610 615 620

Cys Thr Leu Ala Ala Leu Gly Ala Ser Lys Leu Leu Lys Thr Leu Ala  
 625 630 635 640

Lys Val Lys Asn Asp Ile Asn Ala Ala Gly Glu Ser Glu Glu Leu Ala  
 645 650 655

Asn Glu Tyr Glu Thr Arg Ala Val Glu Leu Phe Thr Glu Cys Tyr Ser  
 660 665 670

Ser Asp Glu Asp Leu Ala Glu Gln Leu Leu Val Tyr Ser Cys Glu Ala  
 675 680 685

Trp Gly Gly Ser Asn Cys Leu Glu Leu Ala Val Glu Ala Thr Asp Gln  
 690 695 700

His Phe Ile Ala Gln Pro Gly Val Gln  
 705 710

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 <211> 94  
 <212> PRT  
 <213> Homo sapiens  
  
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 20 25 30  
  
 Leu Trp Tyr Tyr Val Ala Phe Phe Thr Ser Pro Phe Val Val Phe Ser  
 35 40 45  
  
 Trp Asn Val Val Phe Tyr Ile Ala Phe Leu Leu Leu Phe Ala Tyr Val  
 50 55 60  
  
 Leu Leu Met Asp Phe His Ser Val Pro His Pro Pro Glu Leu Val Leu  
 65 70 75 80  
  
 Tyr Ser Leu Val Phe Val Leu Phe Cys Asp Glu Val Arg Gln  
 85 90

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 <211> 586  
 <212> PRT  
 <213> Homo sapiens  
  
 <220>  
 <223> exons 17-28 of PBH1  
  
 <400> 37  
 Met Glu Gln Gly Val Ala Leu Val Glu Glu Ala Arg Ala Ala Gln Glu  
 1 5 10 15  
  
 Pro Thr Glu Gly Val Gly Ser Gly Met Val Gly Cys Arg Ser Arg  
 20 25 30  
  
 Ala Leu Pro His Gly Lys Ala Ala Thr Ala Arg Pro Gly Ser Arg Ser  
 35 40 45  
  
 Arg His Ser Phe His Thr Ser Leu Gln Ala Glu Gly Ala Ser Ser Gly  
 50 55 60  
  
 Leu Gly Gln Pro Arg Lys Gly Leu Pro Gln Cys Ser Gly Gly Leu Lys  
 65 70 75 80  
  
 Gly Ser Ser Ser Ala Ala Lys Val Gly Ala Gln Ala Glu Glu Val Pro  
 85 90 95  
  
 Arg Ala Ser Glu Gly Cys Glu Asp Cys Gln His Ala Val Thr Ser Gln  
 100 105 110  
  
 Lys Arg Lys Gly Leu Ala Asp Val Leu Ser Arg Thr Gly Asn Asn Trp  
 115 120 125

Asp Ser Val Cys Pro Thr Ser Gly Trp Tyr Val Asn Gly Val Asn Tyr  
 130 135 140  
 Phe Thr Asp Leu Trp Asn Val Met Asp Thr Leu Gly Leu Phe Tyr Phe  
 145 150 155 160  
 Ile Ala Gly Ile Val Phe Arg Leu His Ser Ser Asn Lys Ser Ser Leu  
 165 170 175  
 Tyr Ser Gly Arg Val Ile Phe Cys Leu Asp Tyr Ile Ile Phe Thr Leu  
 180 185 190  
 Arg Leu Ile His Ile Phe Thr Val Ser Arg Asn Leu Gly Pro Lys Ile  
 195 200 205  
 Ile Met Leu Gln Arg Met Thr Ser Ile Glu Met Ser Ser Ser Gly Ser  
 210 215 220  
 Ser Ile Pro Thr Leu Arg Phe Phe Glu Phe Val Val Leu Ile Gln Ser  
 225 230 235 240  
 Ile Ser Gly Thr Ser Ser His His Glu Val Met Leu Ser Asp Arg Cys  
 245 250 255  
 Val Leu Leu Pro Val Pro Leu Cys Gly Val Asp Gly Gly Leu Cys Val  
 260 265 270  
 Ala Arg Gln Gly Ile Leu Arg Gln Asn Glu Gln Arg Trp Arg Trp Ile  
 275 280 285  
 Phe Arg Ser Val Ile Tyr Glu Pro Tyr Leu Ala Met Phe Gly Gln Val  
 290 295 300  
 Pro Ser Asp Val Asp Gly Thr Thr Tyr Asp Phe Ala His Cys Thr Phe  
 305 310 315 320  
 Thr Gly Asn Glu Ser Lys Pro Leu Cys Val Glu Leu Asp Glu His Asn  
 325 330 335  
 Leu Pro Arg Phe Pro Glu Trp Ile Thr Ile Pro Leu Val Cys Ile Tyr  
 340 345 350  
 Met Leu Ser Thr Asn Ile Leu Leu Val Asn Leu Leu Val Ala Met Phe  
 355 360 365  
 Gly Cys Val Ala Gly Gly Leu Val Gln Val Leu Asp Phe Gly Thr Glu  
 370 375 380  
 Asn Asn Leu Lys Val Ser Gln Lys Gln Lys Gln Ala Arg Glu Leu Thr  
 385 390 395 400  
 Ala Lys Pro Lys Tyr Thr Leu Ala Ala Ala Gly Phe Arg Arg Trp Thr  
 405 410 415  
 Ser Ala Val Thr Ala Cys Leu Gln Pro Ala Arg Cys Leu Pro Gly Thr  
 420 425 430  
 Gly Arg Gln Gly His Lys Ile Ser Leu Glu Met His Lys Gly Lys Ile  
 435 440 445

Ala Glu Phe Ser Gln Gly Gln His Gln Met Ala Thr Gly Cys Gln Gly  
 450 455 460  
 Asp Phe Lys Asn His Leu Arg Trp Gly Gly Tyr Thr Val Gly Thr Val  
 465 470 475 480  
 Gln Glu Asn Asn Asp Gln Val Trp Lys Phe Gln Arg Tyr Phe Leu Val  
 485 490 495  
 Gln Glu Tyr Cys Ser Arg Leu Asn Ile Pro Phe Pro Phe Ile Val Phe  
 500 505 510  
 Ala Tyr Phe Tyr Met Val Val Lys Lys Cys Phe Lys Cys Cys Cys Lys  
 515 520 525  
 Glu Lys Asn Met Glu Ser Ser Val Cys Ser Val Glu Ala Gly Glu Asp  
 530 535 540  
 Ala Tyr Asn Tyr Arg Glu His Lys Glu Gly Ser Lys Glu Leu Phe Gly  
 545 550 555 560  
 Ser Gln Cys Ala Leu Met Leu Val Phe Ala Ala Thr Leu Ile Arg Cys  
 565 570 575  
 Leu Phe Tyr Leu Glu Gly Ile Gly Asn Ala  
 580 585

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 receptor transmembrane protein extracellular  
 domain conserved motif  
  
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 primer  
  
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168-180 from PBH1 exons 17-28, extracellular  
region used to generate therapeutic antibodies

<400> 40  
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<210> 41  
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<212> PRT  
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<220>  
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region used to generate therapeutic antibodies

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1 5 10 15

Arg Ser Val Ile Tyr Glu Pro Tyr Leu Ala Met Phe Gly Gln Val Pro  
20 25 30

Ser Asp Val Asp Gly Thr Thr Tyr Asp Phe Ala His Cys Thr Phe Thr  
35 40 45

Gly Asn Glu Ser Lys Pro Leu Cys Val Glu Leu Asp Glu His Asn Leu  
50 55 60

Pro Arg Phe Pro  
65

<210> 42  
<211> 41  
<212> PRT  
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<220>  
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520-560 from PBH1 exons 17-28, extracellular  
region used to generate therapeutic antibodies

<400> 42  
Lys Lys Cys Phe Lys Cys Cys Cys Lys Glu Lys Asn Met Glu Ser Ser  
1 5 10 15

Val Cys Ser Val Glu Ala Gly Glu Asp Ala Tyr Asn Tyr Arg Glu His  
20 25 30

Lys Glu Gly Ser Lys Glu Leu Phe Gly  
35 40